AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Previously presented) A recombination system comprising:

a transgenic recombination construct capable of being inserted into the chromosomal DNA of a eukaryotic organism said construct comprising in a 5'- to 3'-orientation;

a first homology sequence A;

at least one recognition sequence for site-directed induction of DNA double-strand breaks; and

a second homology sequence B,

where all recognition sequences for site-directed induction of DNA double-strand breaks are located between homology sequences A and B;

wherein the homology sequences A and B have at least 20 base pairs and at least 70% homology that allows for homologous recombination to each other; and

an enzyme suitable for inducing DNA double-strand breaks at a recognition sequence for the site-directed induction of DNA double-strand breaks or a nucleic acid sequence encoding said enzyme;

wherein after homologous recombination of homology sequences A and B the resulting transgenic sequence derived from said transgenic recombination construct does not comprise any recognition site for said enzyme suitable for inducing DNA double-strand breaks.

2. (Previously presented) The system of claim 1, wherein the construct, after said first homology sequence, contains a further nucleic acid sequence.

3. (Previously presented) The system of claim 2, wherein the construct further contains a second recognition sequence for the site-directed induction of DNA double-strand breaks.

4. (Previously presented) The system of claim 2, wherein the further nucleic acid sequence contains at least one selection marker.

5. (Previously presented) The system of claim 1, wherein the construct further contains at least one of the elements selected from the group consisting of selection markers, reporter genes,

replication origins, multiple cloning regions, border sequences for Agrobacterium transfection, sequences which enable homologous recombination or insertion into a genome of a host organism, expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks and combinations thereof.

6. (Previously presented) The system of claim 1, wherein the enzyme is selected from the group consisting of restriction endonucleases, homing endonucleases, group II intron endonucleases, recombinases, transposases, chimeric nucleases and combinations thereof.

7. (Previously presented) The system of claim 1, wherein the enzyme is selected from the group consisting of F-SceI, F-SceII, F-SuvI, F-TevI, F-TevII, I-AmaI, I-AniI, I-CeuI, I-CeuAIIP, I-ChuI, I-CmoeI, I-CpaI, I-CpaII, I-CreI, I-CrepsbIP, I-CrepsbIIP, I-CrepsbIIIP, I-CrepsbIVP, I-CsmI, I-CvuI, I-CvuAIP, I-DdiI, I-DdiII, I-DirI, I-DmoI, I-HmuI, I-HmuII, I-HspNIP, I-LlaI, I-MsoI, I-NaaI, I-NanI, I-Nc1IP, I-NgrIP, I-NitI, I-NjaI, I-Nsp236IP, I-PakI, I-PboIP, I-PcuIP, I-PcuAI, I-PcuVI, I-PgrIP, I-PobIP, I-PorI, I-PorIIP, I-PpbIP, I-PpoI, I-SPBetaIP, I-ScaI, I-SceI, I-SceII, I-SceIII, I-SceIV, I-SceV, I-SceVI, I-SceVII, I-SexIP, I-SneIP, I-SpomCP, I-SpomIP, I-SpomIIP, I-SquIP, I-Ssp6803I, I-SthPhiJP, I-SthPhiST3P, I-SthPhiS3bP, I-TdeIP, I-TevI, I-TevII, I-TevIII, I-UarAP, I-UarHGPA1P, I-UarHGPA13P, I-VinIP, I-ZbiIP, PI-MtuI, PI-MtuHIP, PI-MtuHIIP, PI-PfuI, PI-PfuII, PI-PkoI, PI-PkoII, PI-PspI, PI-Rma43812IP, PI-SPBetaIP, PI-SceI, PI-TfuI, PI-TfuII, PI-ThyI, PI-ThiI, PI-ThiII and combinations thereof.

8. (Currently amended) The system of claim 1, wherein the enzyme is selected from the group consisting of enzymes ~~encoded by~~ comprising the sequence as shown in SEQ ID NO: 2, 4, 6, 8 or 10, and combinations thereof.

9 (Previously presented) The system of claim 1, wherein the enzyme is expressed from an expression cassette that contains a nucleic acid sequence encoding said enzyme.

10. (Previously presented) The system of claim 9, wherein the nucleic acid sequence comprises the sequence as shown in SEQ ID NO. 1, 3, 5, 7 or 9.

11. (Previously presented) A method for removing a DNA sequence from chromosomal DNA of a eukaryotic cell or organism comprising:

introducing the recombination system of claim 1 into the chromosomal DNA of a eukaryotic cell or organism;

inducing DNA double-strand breaks at the recognition sequence; and

conducting homologous recombination between the homology sequences A and B.

12. (Previously presented) The method of claim 11, wherein the construct contains a further nucleic acid sequence.

13. (Cancelled).

14. (Previously presented) The method of claim 11, wherein the construct, after said first homology sequence A contains a second recognition sequence for the site-directed induction of DNA double-strand breaks.

15. (Previously presented) The method of claim 11, wherein the construct contains at least one of the elements selected from the group consisting of selection markers, reporter genes, replication origins, multiple cloning regions, border sequences for Agrobacterium transfection, sequences which enable homologous recombination or insertion into a genome of a host organism, expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks and combinations thereof.

16. (Previously presented) The method of claim 11, wherein the enzyme is selected from the group consisting of restriction endonucleases, homing endonucleases, recombinases, transposases, chimeric nucleases and combinations thereof.

17. (Previously presented) The method of claim 11, wherein the enzyme is selected from the group consisting of F-SceI, F-SceII, F-SuvI, F-TevI, F-TevII, I-AmaI, I-AniI, I-CeuI, I-CeuAIIP, I-ChuI, I-CmoeI, I-CpaI, I-CpaII, I-CreI, I-CrepsbIP, I-CrepsbIIP, I-CrepsbIIIP, I-CrepsbIVP, I-CsmI, I-CvuI, I-CvuAIP, I-DdiI, I-DdiII, I-DirI, I-DmoI, I-HmuI, I-HmuII, I-

HspNIP, I-LlaI, I-MsoI, I-NaaI, I-NanI, I-Nc1IP, I-NgrIP, I-NitI, I-NjaI, I-Nsp236IP, I-PakI, I-PboIP, I-PcuIP, I-PcuAI, I-PcuVI, I-PgrIP, I-PobIP, I-PorI, I-PorIIP, I-PpbIP, I-PpoI, I-SPBetaIP, I-ScaI, I-SceI, I-SceII, I-SceIII, I-SceIV, I-SceV, I-SceVI, I-SceVII, I-SexIP, I-SneIP, I-SpomCP, I-SpomIP, I-SpomIIP, I-SquIP, I-Ssp6803I, I-SthPhiJP, I-SthPhiST3P, I-SthPhiS3bP, I-TdeIP, I-TevI, I-TevII, I-TevIII, I-UarAP, I-UarHGPA1P, I-UarHGPA13P, I-VinIP, I-ZbiIP, PI-MtuI, PI-MtuHIP, PI-MtuHIIP, PI-PfuI, PI-PfuII, PI-PkoI, PI-PkoII, PI-PspI, PI-Rma43812IP, PI-SPBetaIP, PI-SceI, PI-TfuI, PI-TfuII, PI-ThyI, PI-TliI, PI-TliII and combinations thereof.

18. (Previously presented) The method of claim 11, wherein the enzyme is selected from the group consisting of enzymes that contain the sequence as shown in SEQ ID NO: 2, 4, 6, 8 or 10, and combinations thereof.

19. (Previously presented) The method of claim 11, wherein the enzyme is encoded in an expression cassette.

20. (Previously presented) The method of claim 11, wherein the nucleic acid sequence comprises the sequence as shown in SEQ ID NO: 1, 3, 5, 7 or 9, or a combination thereof.

21. (Previously presented) An organism comprising the recombination system of claim 1.

22. (Previously presented) The organism of claim 21 selected from the group consisting of yeasts, algae, fungi and animal and plant organisms.

23. (Cancelled).

24. (Previously presented) The organism of claim 22, wherein the plant organism is selected from the group consisting of *Arabidopsis thaliana*, tobacco, wheat, rye, barley, oats, oilseed rape, maize, potato, sugar beet, soybean, sunflower, pumpkin, squash, and peanut.

25. (Currently amended) A cell, cell culture, organ, tissue, part or transgenic propagation material comprising the ~~recombinant~~ recombination system of claim 1.

26. (Cancelled).

27. (Previously presented) The system of claim 2, wherein the further nucleic acid sequence comprises an expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks.

28. (Previously presented) The system of claim 1, wherein the construct further comprises an expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks.

29. (Previously presented) The method of claim 12, wherein the further nucleic acid sequence comprises an expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks.

30. (Previously presented) The method of claim 11, wherein the construct comprises an expression cassette for an enzyme suitable for inducing DNA double-strand breaks at the recognition sequence for the site-directed induction of DNA double-strand breaks.

31. (New) The recombination system of claim 1, wherein the eukaryotic organism is a plant organism.

32. (New) The method of claim 11, wherein the eukaryotic cell or organism is a plant cell or plant organism.